

B. Zeman

1645

P#13

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/461,580A

DATE: 11/13/2000
TIME: 13:26:36

Input Set : A:\0050.1618-000.txt
Output Set: N:\CRF3\11132000\I461580A.raw

4 <110> APPLICANT: Guarente, Leonard
5 Imai, Shin-ichiro
6 Armstrong, Christopher
8 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
9 ALTER HISTONE PROTEIN ACETYLATION, DECREASE AGING, INCREASE
10 LIFESPAN
12 <130> FILE REFERENCE: 0050.1618-000
14 <140> CURRENT APPLICATION NUMBER: 09/461,580A
15 <141> CURRENT FILING DATE: 1999-12-15
17 <160> NUMBER OF SEQ ID NOS: 35
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 737
23 <212> TYPE: PRT
24 <213> ORGANISM: Mus musculus
26 <400> SEQUENCE: 1
27 Met Ala Asp Glu Val Ala Leu Ala Leu Gln Ala Ala Gly Ser Pro Ser
28 1 5 10 15
29 Ala Ala Ala Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu
30 20 25 30
31 Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly
32 35 40 45
33 Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala
34 50 55 60
35 Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala
36 65 70 75 80
37 Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly
38 85 90 95
39 Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe
40 100 105 110
41 Asp Asp Asp Glu Gly Glu Glu Glu Asp Glu Ala Ala Ala Ala Ala
42 115 120 125
43 Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu
44 130 135 140
45 Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Arg Thr
46 145 150 155 160
47 Ser His Ala Ser Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro
48 165 170 175
49 Tyr Thr Phe Val Glu Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr
50 180 185 190
51 Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp
52 195 200 205
53 Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro
54 210 215 220
55 Lys Arg Lys Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys
56 225 230 235 240
57 Leu Leu Gln Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val

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TECH CENTER 1600/2000

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DATE: 11/13/2000

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TIME: 13:26:36

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58          245          250          255
59 Ser Val Ser Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr
60          260          265          270
61 Ala Arg Leu Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met
62          275          280          285
63 Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe
64          290          295          300
65 Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys
66 305          310          315          320
67 Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr
68          325          330          335
69 Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu
70          340          345          350
71 Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr
72          355          360          365
73 Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val
74          370          375          380
75 Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys
76 385          390          395          400
77 Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg
78          405          410          415
79 Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly
80          420          425          430
81 Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro
82          435          440          445
83 His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu
84          450          455          460
85 His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu
86 465          470          475          480
87 Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro
88          485          490          495
89 Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu
90          500          505          510
91 Leu Val His Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu
92          515          520          525
93 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile
94          530          535          540
95 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu
96 545          550          555          560
97 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr
98          565          570          575
99 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala
100          580          585          590
101 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu
102          595          600          605
103 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser
104          610          615          620
105 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr
106 625          630          635          640

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```

107 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu
108                               645          650          655
109 Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser
110                               660          665          670
111 Pro Ser Leu Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe
112                               675          680          685
113 Tyr Asn Gly Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly
114                               690          695          700
115 Ser Gly Phe Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala
116 705                               710          715          720
117 Ile Ala Thr Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys
118                               725          730          735
119 Ser
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 272
125 <212> TYPE: PRT
126 <213> ORGANISM: Saccharomyces cerevisiae
128 <400> SEQUENCE: 2
129 Ile Asn Lys Val Leu Cys Thr Arg Leu Arg Leu Ser Asn Phe Phe Thr
130 1                               5          10          15
131 Ile Asp His Phe Ile Gln Lys Leu His Thr Ala Arg Lys Ile Leu Val
132                               20          25          30
133 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
134                               35          40          45
135 Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly Leu Asp Asp
136 50                               55          60
137 Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp Pro Ser Val
138 65                               70          75          80
139 Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Glu Lys Ile Tyr Ser
140                               85          90          95
141 Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly Lys Leu Leu
142                               100         105         110
143 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
144                               115         120         125
145 Ser Thr Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Thr
146 130                               135         140
147 Cys Val Thr Cys His Trp Asn Leu Pro Gly Glu Arg Ile Phe Asn Lys
148 145                               150         155         160
149 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Lys Lys Arg
150                               165         170         175
151 Arg Glu Tyr Phe Pro Glu Gly Tyr Asn Asn Lys Val Gly Val Ala Ala
152                               180         185         190
153 Ser Gln Gly Ser Met Ser Glu Arg Pro Pro Tyr Ile Leu Asn Ser Tyr
154                               195         200         205
155 Gly Val Leu Lys Pro Asp Ile Thr Phe Phe Gly Glu Ala Leu Pro Asn
156 210                               215         220
157 Lys Phe His Lys Ser Ile Arg Glu Asp Ile Leu Glu Cys Asp Leu Leu
158 225                               230         235         240
159 Ile Cys Ile Gly Thr Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val

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160                               245                               250                               255
161 Asn Met Val Pro Ser His Val Pro Gln Val Leu Ile Asn Arg Asp Pro
162                               260                               265                               270
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 267
167 <212> TYPE: PRT
168 <213> ORGANISM: Saccharomyces cerevisiae
170 <400> SEQUENCE: 3
171 Ile Asn Lys Val Leu Ser Thr Arg Leu Arg Leu Pro Asn Phe Asn Thr
172 1                               5                               10                               15
173 Ile Asp His Phe Thr Ala Thr Leu Arg Asn Ala Lys Lys Ile Leu Val
174                               20                               25                               30
175 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
176                               35                               40                               45
178 Ser Ser Glu Gly Phe Tyr Ser Ser Lys Ile Arg His Leu Gly Leu Glu Asp
179                               50                               55                               60
180 Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp Pro Ser Val
181 65                               70                               75                               80
182 Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn Met Tyr Ser
183                               85                               90                               95
184 Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly Lys Leu Leu
185                               100                              105                              110
186 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
187                               115                              120                              125
188 Asp Pro Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Ser
189                               130                              135                              140
190 Cys Val Thr Cys His Trp Gln Ile Pro Gly Glu Lys Ile Phe Glu Asn
191 145                              150                              155                              160
192 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Gln Lys Arg
193                               165                              170                              175
194 Lys Gln Tyr Phe Pro Met Ser Asn Gly Asn Asn Thr Val Gln Thr Asn
195                               180                              185                              190
196 Ile Asn Phe Asn Ser Pro Ile Leu Lys Ser Tyr Gly Val Leu Lys Pro
197                               195                              200                              205
198 Asp Met Thr Phe Phe Gly Glu Ala Leu Pro Ser Arg Phe His Lys Thr
199                               210                              215                              220
200 Ile Arg Lys Asp Ile Leu Glu Cys Asp Leu Leu Ile Cys Ile Gly Thr
201 225                              230                              235                              240
202 Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val Asn Met Val Pro Ser
203                               245                              250                              255
204 His Val Pro Gln Ile Leu Ile Asn Arg Asp Met
205                               260                              265
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 245
210 <212> TYPE: PRT
211 <213> ORGANISM: Mus musculus
213 <400> SEQUENCE: 4
214 Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp
215 1                               5                               10                               15

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Input Set : A:\0050.1618-000.txt
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```

216 Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys
217           20           25           30
218 Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro
219           35           40           45
220 Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe
221           50           55           60
222 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg
223 65           70           75           80
224 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly
225           85           90           95
226 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys
227           100          105          110
228 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu
229           115          120          125
230 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala
231           130          135          140
232 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val
233 145          150          155          160
234 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro
235           165          170          175
237 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly
238           180          185          190
239 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp
240           195          200          205
241 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro
242           210          215          220
243 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu
244 225          230          235          240
245 Ile Asn Arg Glu Pro
246           245
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 237
251 <212> TYPE: PRT
252 <213> ORGANISM: Escherichia coli
254 <400> SEQUENCE: 5
255 Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser
256 1           5           10           15
257 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu
258           20           25           30
259 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Phe Ala Arg Asn
260           35           40           45
261 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln
262           50           55           60
263 Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu
264 65           70           75           80
265 Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp
266           85           90           95
267 Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly
268           100          105          110

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PI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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DATE: 11/13/2000

TIME: 13:26:37

Input Set : A:\0050.1618-000.txt

Output Set: N:\CRF3\11132000\I461580A.raw

L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27

L:1266 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 34